

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
ATGCGCGCCT	CCGGCTGGG	GCTGCTGGG	CTGCTGCTAC	CGCTGCTGTG	GCTACTGTTG	60
MetProProS	erGlyLeuAr	gLeuLeuPro	LeuLeuLeuP	roLeuLeuTr	pLeuLeuVal	
CTGAGCGCTG	GCGCGCGGC	CGCGGACTA	TCCACTGCA	AGACTATCGA	CATGGAGCTG	120
LeuThrProG	lyProProAl	aAlaGlyLeu	SerThrCysL	ysThrIleAs	pMetGluLeu	
GTAAGCGGA	AGCGCATCGA	GCGCATCGC	GCCAGATCC	TGTOCAAGCT	GCGGCTCGCC	180
VallLysArgL	ysArgIleGl	uAlaIleArg	GlyGlnIleL	euSerLysLe	uArgLeuAla	
AGCCCCCGA	GCCAGGGGA	GGTGGCGCC	GCGCGCTGC	CCGAGCGGT	GCTGCGCTG	240
SerProProS	erGlnGlyGl	uValProPro	GlyProLeuP	roGluAlaVa	lLeuAlaLeu	
TACAACAGCA	CCCGGACCG	GGTGGCGGG	GAGAGTGCAG	AACCGGAGCC	CGAGCTGAG	300
TyrAsnSerT	hrArgAspAr	gValAlaGly	GluSerAlaG	luProGluPr	oGluProGlu	
GCGACTACT	ACGCCAAGGA	GGTCACCGC	GTCCTAATGG	TGGAACCCA	CAACGAATC	360
AlaAspTyrT	yrAlaLysGl	uValThrArg	VallLeuMetV	alGluThrHi	sAsnGluIle	
TATGACAAGT	TCAAGCAGAG	TACACACAGC	ATATATATGT	TCTTCAACAC	ATCAGAGCTC	420
TyrAspLysP	heLysGlnSe	rThrHisSer	IleTyrMetP	hePheAsnTh	rSerGluLeu	
CGAGAAGCGG	TACCIGAACC	CGTGTTGCTC	TCCCGGCAG	AGCTGGTCT	GCTGAGGAGG	480
ArgGluAlaV	alProGluPr	oValLeuLeu	SerArgAlaG	luLeuArgLe	uLeuArgArg	
CTCAAGTTAA	AAGTGGAGCA	GCACTGGAG	CTGTACCAGA	AATACAGCAA	CAATTCTGG	540
LeuLysLeuL	ysValGluGl	nHisValGlu	LeuTyrGlnL	ysTyrSerAs	nAsnSerTrp	
CGATACTCA	GCAACCGCT	GCTGGCACC	AGGACTGCG	CAGAGTGGTT	ATCTTTTGAT	600
ArgTyrLeuS	erAsnArgLe	uLeuAlaPro	SerAspSerP	roGluTrpLe	uSerPheAsp	
GTCACCGGAG	TGTGGGGCA	GTCGTTGAGC	CGTGGAGGG	AAATTGAGGG	CTTTGGCTT	660
ValThrGlyV	alValArgGl	nTrpLeuSer	ArgGlyGlyG	luIleGluGl	yPheArgLeu	
AGCGCCACT	GCTGCTGTA	CAGCAGGAT	AACACACTGC	AAGTGGACAT	CAACGGTTC	720
SerAlaHisC	ysSerCysAs	pSerArgAsp	AsnThrLeuG	InValAspIl	eAsnGlyPhe	
ACTACCGGC	GCGAGGTGA	CCTGGCCACC	ATTCATGGCA	TGAACCGGC	TTTCTGCTT	780
ThrThrGlyA	rgArgGlyAs	pLeuAlaThr	IleHisGlyM	etAsnArgPr	oPheLeuLeu	
CTCATGGCCA	CCCGCTGGA	GAGGGCCAG	CATCTGCAA	GCGAATTGG	GGAGGCGGA	840
LeuMetAlaT	hrProLeuGl	uArgAlaGln	HisLeuGlnS	erGluPheGl	yGlyGlyGly	
TTCCCGCTCG	GGCTTTGGGC	GGGAGGGGC	TCAAGCGCG	CAATCAACTA	TAAGCAGCTC	900
SerProLeuG	lyLeuTrpAl	aGlyGlyGly	SerAlaAlaA	laIleAsnTy	rllysGlnLeu	
CAGCTCCAG	AAAGGAGAA	CATTGGGAA	TGTCAGGAGC	TOCTGGAGCA	GCTGAATGGA	960
GlnLeuGlnG	luArgThrAs	nIleArgLys	CysGlnGluL	euLeuGluGl	nLeuAsnGly	

Fig. 1

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
AAGATCAACC	TCACTACAG	GGGGACTTC	AAGATCOCTA	TGGAGATGAC	GGAGAAGATG	1020
LysIleAsnL	euIhrTyrAr	gAlaAspPhe	LysIleProM	etGluMetTh	rGluLysMet	
CAGAAGAGTT	ACACTGCCIT	TGCCATCCAA	GAGATGCTCC	AGAATGICTT	TCTTGTCTTC	1080
GlnLysSerT	yrThrAlaPh	eAlaIleGln	GluMetLeuG	InAsnValPh	eLeuValPhe	
AGAAACAATT	TCTCCAGCAC	TGGGTGGAAT	GAGACTATTG	TTGTACGICT	OCTGGATGAA	1140
ArgAsnAsnP	heSerSerTh	rGlyTrpAsn	GluThrIleV	alValArgLe	uLeuAspGlu	
CTCCACCAGC	AGACAGIGIT	TCTGAAGACA	GTACTAGAGG	AAAAGCAAGA	GGAAAGATIG	1200
LeuHisGlnG	InThrValPh	eLeuLysThr	ValLeuGluG	luLysGlnGl	uGluArgLeu	
AAGTGGGAGA	TGTCTCAAC	TGCCTCCAC	TTGAAGAGCT	ATTACTGCAG	GGTCCAAAGG	1260
ThrTrpGluM	etSerSerTh	rAlaLeuHis	LeuLysSerT	yrTyrTrpAr	gValGlnArg	
TACCTTAAAC	TCATGAAGTA	CAACAGCTAC	GCTGGATGG	TGGTCCGAGC	AGAGATCTTC	1320
TyrLeuLysL	euMetLysTy	rAsnSerTyr	AlaTrpMetV	alValArgAl	aGluIlePhe	
AGGAACCTTC	TCATCATTCG	AAGACTTACC	AGAAACTTCC	AAAACGATC	TAGAAC	1376
ArgAsnPheL	euIleIleAr	gArgLeuThr	ArgAsnPheG	InAsn...Se	rArg	
				uga		

ifn+MMP+TGFB Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
ATGAACAACA	GGTGGATCCT	CCAGCTGGC	TTCCTGCTGT	GCTTCTCCAC	CACAGCCCTC	60
MetAsnAsnA	rgTrpIleLe	uHisAlaAla	PheLeuLeuC	ysPheSerTh	rThrAlaLeu	
TCCATCAACT	ATAAGCAGCT	CCAGCTCCAA	GAAAGGAAGA	ACATTGGGAA	ATGTCAGGAG	120
SerIleAsnT	yrLysGlnLe	uGlnLeuGln	GluArgThrA	snIleArgLy	sCysGlnGlu	
CTCTGGAGC	AGCTGAATGG	AAAGATCAAC	CTCACTTACA	GGGGGACTTT	CAAGATCCCT	180
LeuLeuGluG	InLeuAsnG	yLysIleAsn	LeuThrTyrA	rgAlaAspPh	eLysIlePro	
ATGGAGATGA	CGGAGAAGAT	GCAGAAGAGT	TACACTGGCT	TGGCATCCA	AGAGATGCTC	240
MetGluMetT	hrGluLysMe	tGlnLysSer	TyrThrAlaP	heAlaIleG	nGluMetLeu	
CAGATGTCT	TTCCTGTCTT	CAGAAACAAT	TTCTCCAGCA	CTGGGTGGAA	TCAGACTATT	300
GlnAsnValP	heLeuValPh	eArgAsnAsn	PheSerSerT	hrGlyTrpAs	nGluThrIle	
GTGTAGTIC	TCTGGATGA	ACTCCACCAG	CAGACAGTGT	TTCTGAAGAC	AGTACTAGAG	360
ValValArgL	euLeuAspG	uLeuHisGln	GlnThrValP	heLeuLysTh	rValLeuGlu	
GAAAAGCAAG	AGGAAAGATT	GACGTGGGAG	ATGTCTTCAA	CTGCTCTCCA	CTTGAAGAGC	420
GluLysGlnG	luGluArgLe	uThrTrpGlu	MetSerSerT	hrAlaLeuHi	sLeuLysSer	
TATTACTGGA	GGGTGCAAG	GTACCTTAAA	CTCATGAAGT	ACAACAGCTA	CGCTGGGATG	480
TyrTyrTrpA	rgValGlnAr	gTyrLeuLys	LeuMetLysT	yrAsnSerTy	rAlaTrpMet	
GIGGTCCGAG	CAGAGATCTT	CAGGAACITT	CTCATCATTC	GAAGACTTAC	CAGAAACTTC	540
ValValArgA	laGluIlePh	eArgAsnPhe	LeuIleIleA	rgArgLeuTh	rArgAsnPhe	
CAAAACGAAT	TGCGGGGAGG	CGGATCCCGG	CTCGGCTTTT	GGGCGGGAGG	GGGCTCAGCG	600
GlnAsnGluP	heGlyGlyG	yGlySerPro	LeuGlyLeuT	rpAlaGlyG	yGlySerAla	
GGCGCACTAT	CCACCTGCCA	GACTATCGAC	ATGGAGCTGG	TGAAGCGGAA	GCGCATCGAG	660
AlaAlaLeuS	erThrCysLy	sThrIleAsp	MetGluLeuV	alLysArgLy	sArgIleGlu	
GCCATCCGCG	GCCAGATCCT	GTCGAAGCTG	CGCTCTGCCA	GGCCCCGAG	CCAGGGGGAG	720
AlaIleArgG	lyGlnIleLe	uSerLysLeu	ArgLeuAlaS	erProProSe	rgInGlyGlu	
GIGGCGCCCG	GGCGGCTGCC	CGAGGCGGIG	CTGGCCCTGT	ACAACAGCAC	CGGCGACCGG	780
ValProProG	lyProLeuPr	oGluAlaVal	LeuAlaLeuT	yrAsnSerTh	rArgAspArg	
GIGGCGGGGG	AGAGTGCAGA	ACCGGAGCCC	GAGCTGAGG	CGGACTACTA	CGGCAAGGAG	840
ValAlaGlyG	luSerAlaG	uProGluPro	GluProGluA	laAspTyrTy	rAlaLysGlu	
GTCACCGCGG	TGCTAATGGT	GGAAACCCAC	AAAGAAATCT	ATGACAAGTT	CAGGCAGAGT	900
ValThrArgV	alLeuMetVa	lGluThrHis	AsnGluIleT	yrAspLysPh	eLysGlnSer	
ACACACAGCA	TATATATGTT	CTTCAACACA	TCAGAGCTCC	GAGAAGCGGT	AACCTGAACC	960
ThrHisSerI	leTyrMetPh	ePheAsnThr	SerGluLeuA	rgGluAlaVa	lProGluPro	

Fig. 2

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10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GTGTGTCTCT	CCCGGCAGA	GCTGGTCTG	CTGAGGAGC	TCAAGTTAA	AGTGGAGCAG	1020
ValLeuLeuS	erArgAlaGl	uLeuArgLeu	LeuArgArgL	eulysLeuLy	sValGluGln	
CAAGTGGAGC	TGTACCAGAA	ATACAGCAAC	AATTCCTGCC	GATACCTCAG	CAACCGGCTG	1080
HisValGluL	eulYrGlnLy	sYrSerAsn	AsnSerTrpA	rgYrLeuSe	rAsnArgLeu	
CTGGCAACCA	GCGACTGGC	AGAGTGGTTA	TCTTTTGATG	TCAACCGAGT	TGTGCGGCAG	1140
LeuAlaProS	erAspSerPr	oGluTrpLeu	SerPheAspV	alThrGlyVa	lValArgGln	
TGGTTGAGCC	GTTGAGGGGA	AATTGAGGGC	TTTGCGCTTA	GCGCCCACTG	CTCTGTGTAC	1200
TrpLeuSerA	rgGlyGlyGl	uLieGluGly	PheArgLeuS	erAlaHisCy	sSerCysAsp	
AGCAGGGATA	ACACACTGCA	AGTGGACATC	AACGGGTTCa	CTAACGGCOG	CGAGGTGAC	1260
SerArgAspA	snThrLeuGl	nValAspIle	AsnGlyPheT	hrThrGlyAr	gArgGlyAsp	
CTGGCCACCA	TTCATGGCAT	GAACCGGCTT	TTCCTGCTTC	TCAATGGCAC	CCCGCTGGAG	1320
LeuAlaThrI	leHisGlyMe	tAsnArgPro	PheLeuLeuL	eMetAlaTh	rProLeuGlu	
AGGCGCCAGC	ATCTGCAAAG	CtgaTCTAGA	CC			1352
ArgAlaGlnH	isLeuGlnSe	r...SerArg				

Protein	Sequence	Reference
MMP-1/MMP-8		
Human type I collagen ($\alpha 1$)	Ala-Pro-Gln-Gly ₇₇₅ ~Ile ₇₇₆ -Ala-Gly-Gln	80
Human type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₅ ~Leu ₇₇₆ -Leu-Gly-Ala	80
Human type II collagen	Gly-Pro-Gln-Gly ₇₇₅ ~Leu ₇₇₆ -Ala-Gly-Gln	80
Human type III collagen	Gly-Pro-Leu-Gly ₇₇₅ ~Ile ₇₇₆ -Ala-Gly-Ile	80
Human α_2 -macroglobulin	Gly-Pro-Glu-Gly ₆₇₉ ~Leu ₆₈₀ -Arg-Val-Gly	84
Rat α_2 -macroglobulin	Ala-Ala-Tyr-His ₆₈₁ ~Leu ₆₈₂ -Val-Ser-Gln	84
Rat α_2 -macroglobulin	Met-Asp-Ala-Phe ₆₉₁ ~Leu ₆₉₂ -Glu-Ser-Ser	84
Rat α_1 -macroglobulin	Glu-Pro-Gln-Ala ₆₈₃ ~Leu ₆₈₄ -Ala-Met-Ser	84
Rat α_1 -macroglobulin	Gln-Ala-Leu-Ala ₆₈₅ ~Met ₆₈₆ -Ser-Ala-Ile	84
Chicken ovostatin	Pro-Ser-Tyr-Phe ₆₇₃ ~Leu ₆₇₄ -Asn-Ala-Gly	79
Human pregnancy zone protein	Tyr-Glu-Ala-Gly ₆₈₅ ~Leu ₆₈₆ -Gly-Val-Val	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₆₈₇ ~Val ₆₈₈ -Val-Glu-Arg	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₇₅₇ ~Ile ₇₅₈ -Ser-Ser-Thr	84
α_1 -Protease inhibitor	Gly-Ala-Met-Phe ₃₅₂ ~Leu ₃₅₃ -Glu-Ala-Ile	85
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	86
Human aggrecan	Thr-Glu-Gly-Glu ₃₇₃ ~Ala ₃₇₄ -Arg-Gly-Ser	86
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₉ ~Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-2		
Guinea pig $\alpha 1$ (I) gelatin	Gly-Ala-Hyp-Gly ₃₄₇ ~Leu ₃₄₈ -Glx-Gly-His	24
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Gln-Gly ₁₉₀ ~Val ₁₉₁ -Arg-Gly-Glu	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₂₇₇ ~Val ₂₇₈ -Gln-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ser-Gly ₃₀₁ ~Leu ₃₀₂ -Hyp-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₃₃₁ ~Glu ₃₃₂ -Arg-Gly-Ser	30
Rat $\alpha 1$ (I) gelatin	Gly-Ala-Lys-Gly ₃₆₁ ~Leu ₃₆₂ -Thr-Gly-Ser	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₃₈₂ ~Gln ₃₈₃ -Asp-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₆₃₄ ~Phe ₆₃₅ -Ala-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ile-Gly ₆₇₆ ~Asn ₆₇₇ -Val-Gly-Ala	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Hyl-Gly ₆₈₅ ~Ser ₆₈₆ -Arg-Gly-Ala	30
Bovine type I collagen ($\alpha 1$)	Gly-Pro-Gln-Gly ₇₇₅ ~Ile ₇₇₆ -Ala-Gly-Gln	22
Bovine type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₅ ~Leu ₇₇₆ -Leu-Gly-Ala	22
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₆₂ ~Tyr ₆₃ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₉ ~Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-3		
Human α_2 -macroglobulin	Gly-Pro-Glu-Gly ₆₇₉ ~Leu ₆₈₀ -Arg-Val-Gly	79
Human α_2 -macroglobulin	Arg-Val-Gly-Phe ₆₈₄ ~Tyr ₆₈₅ -Glu-Ser-Asp	79
Human α_1 -antichymotrypsin	Leu-Leu-Ser-Ala ₃₆₀ ~Leu ₃₆₁ -Val-Glu-Thr	91
α_1 -protease inhibitor	Glu-Ala-Ile-Pro ₃₅₇ ~Met ₃₅₈ -Ser-Ile-Pro	91
Antithrombin III	Ile-Ala-Gly-Arg ₃₂₅ ~Ser ₃₂₆ -Leu-Asn-Pro	91
Chicken ovostatin	Leu-Asn-Ala-Gly ₆₇₇ ~Phe ₆₇₈ -Thr-Ala-Ser	79, 92
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	93
Substance P	Lys-Pro-Gln-Gln ₆ ~Phe ₇ -Phe-Gly-Leu	37
Human ProMMP-1	Asp-Val-Ala-Gln ₈₀ ~Phe ₈₁ -Val-Leu-Thr	43
Human ProMMP-3	Asp-Thr-Leu-Glu ₆₈ ~Val ₆₉ -Met-Arg-Lys	94
Human ProMMP-3	Asp-Val-Gly-His ₈₂ ~Phe ₈₃ -Arg-Thr-Phe	94
Human ProMMP-8	Asp-Ser-Gly-Gly ₇₈ ~Phe ₇₉ -Met-Leu-Thr	95
Human ProMMP-9	Arg-Val-Ala-Glu ₄₀ ~Met ₄₁ -Arg-Gly-Glu	48
Human ProMMP-9	Asp-Leu-Gly-Arg ₈₇ ~Phe ₈₈ -Gln-Thr-Phe	48
Human fibronectin	Pro-Phe-Ser-Pro ₆₈₉ ~Leu ₆₉₀ -Val-Ala-Thr	21

Fig. 4

	Sequence	Reference
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₉ ~Leu ₁₀₀ -Leu-Pro-Ala	88
	Ala-Pro-Gly-Asn ₁₀₉ ~Ala ₁₁₀ -Ser-Glu-Ser	88
	Phe-Ser-Ser-Glu ₁₇₆ ~Ser ₁₇₇ -Lys-Arg-Glu	88
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Ala-Gly-Gly-Ala ₁₁₅ ~Gln ₁₁₆ -Met-Gly-Val	96
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Gln-Met-Gly-Val ₁₁₉ ~Met ₁₂₀ -Gln-Gly-Pro	96
Bovine $\alpha 1$ (IX) collagen, NC2	Met-Ala-Ala-Ser~Leu-Lys-Arg-Pro	96
Bovine $\alpha 2$ (IX) collagen, NC2	~Ala-Lys-Arg-Glu	96
Bovine $\alpha 3$ (IX) collagen, NC2	~Leu-Arg-Lys-Pro	96
Bovine $\alpha 1$ (XI) collagen, N-telopeptide	Gln-Ala-Gln-Ala~Ile-Leu-Gln-Gln	96
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Bovine insulin, B chain	Leu-Val-Glu-Ala ₁₄ ~Leu ₁₅ -Tyr-Leu-Val	97
Bovine insulin, B chain	Glu-Ala-Leu-Tyr ₁₆ ~Leu ₁₇ -Val-Cys-Gly	21, 97
MMP-7		
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87
Human prourokinase	Pro-Pro-Glu-Glu ₁₄₃ ~Leu ₁₄₄ -Lys-Phe-Gln	98
MMP-9		
Human type V collagen ($\alpha 1$)	Gly-Pro-Pro-Gly ₄₃₉ ~Val ₄₄₀ -Val-Gly-Pro	99
Human type V collagen ($\alpha 2$)	Gly-Pro-Pro-Gly ₄₄₅ ~Leu ₄₄₆ -Arg-Gly-Glu	99
Human type XI collagen ($\alpha 1$)	Gly-Pro-Gly-Gly ₄₃₉ ~Val ₄₄₀ -Val-Gly-Pro	99
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₆₂ ~Tyr ₆₃ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
MMP-10		
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87

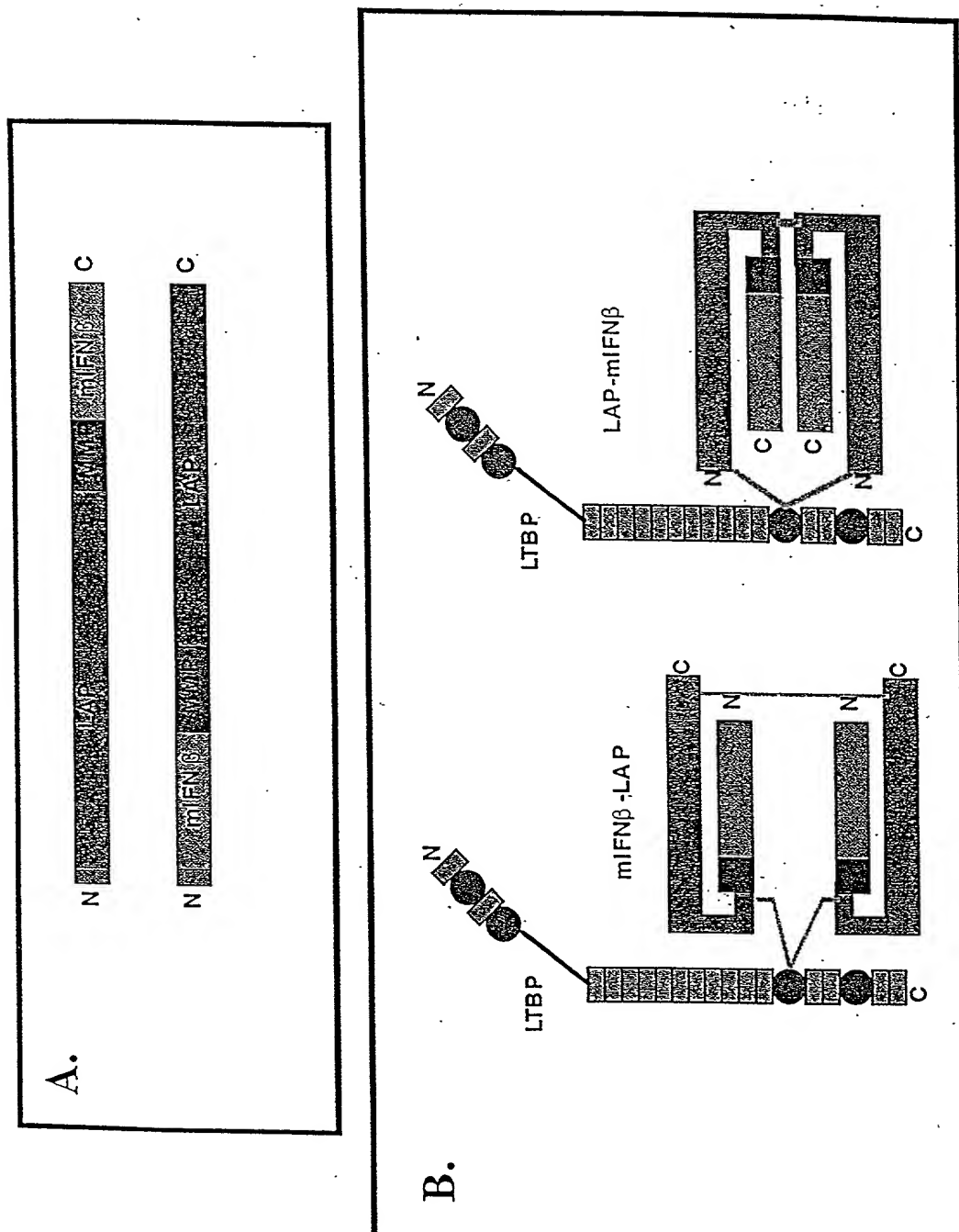


Fig. 5

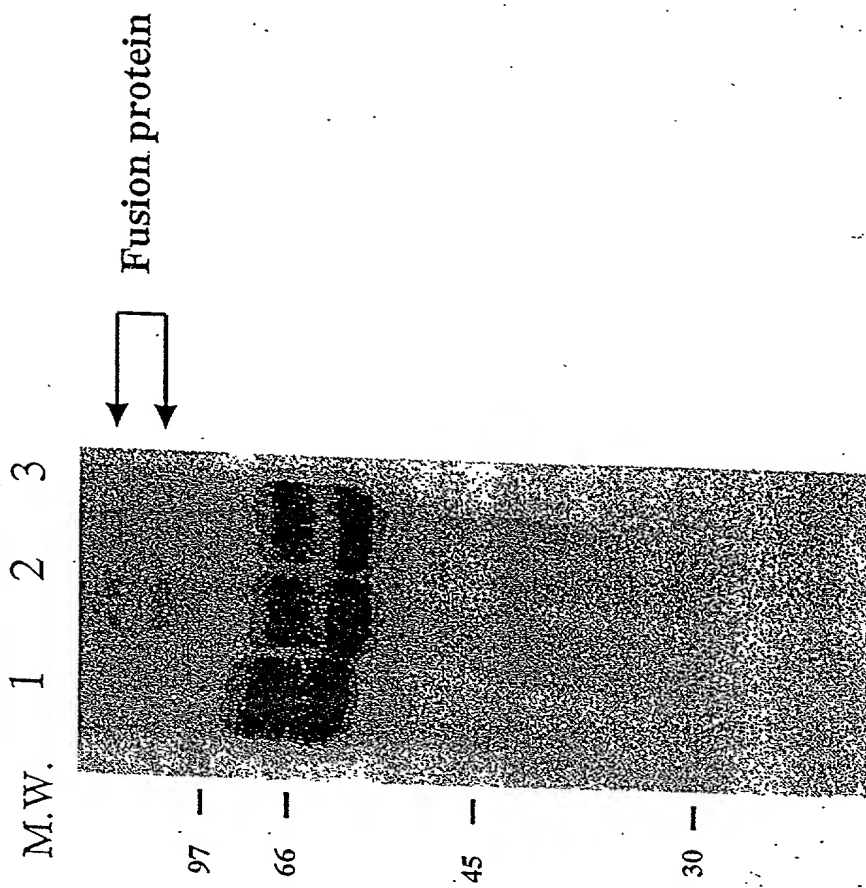


Fig. 6

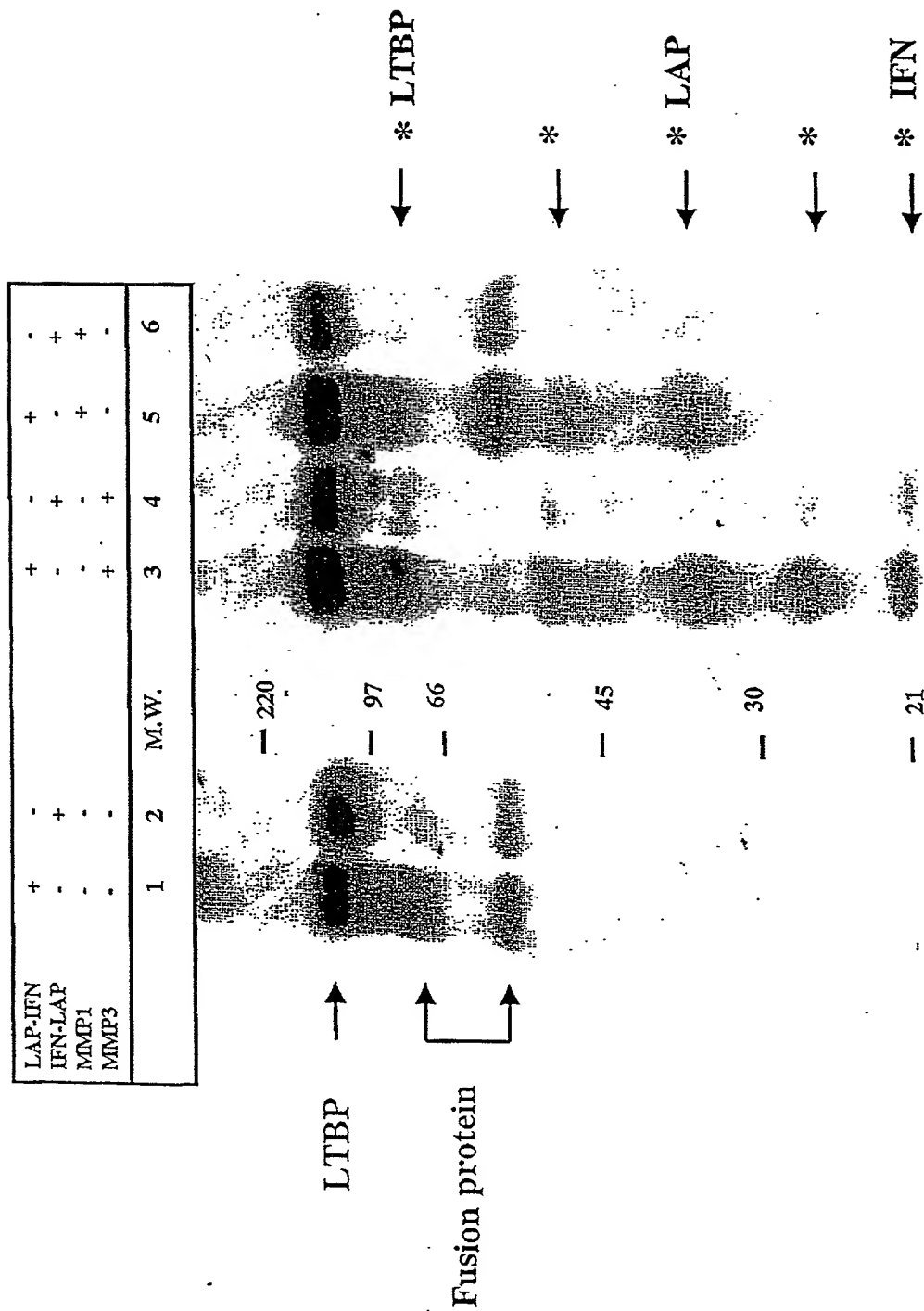
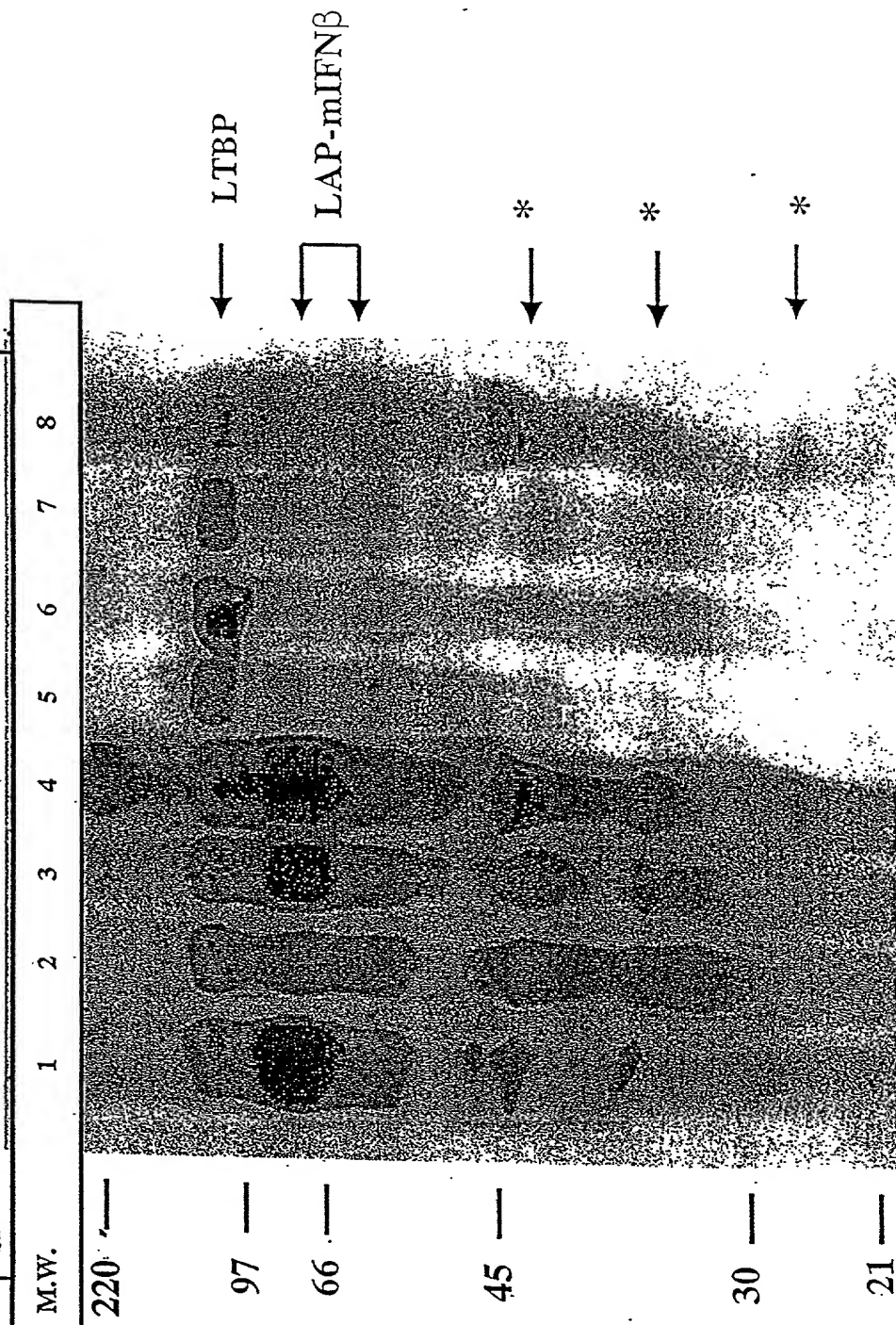


Fig. 7



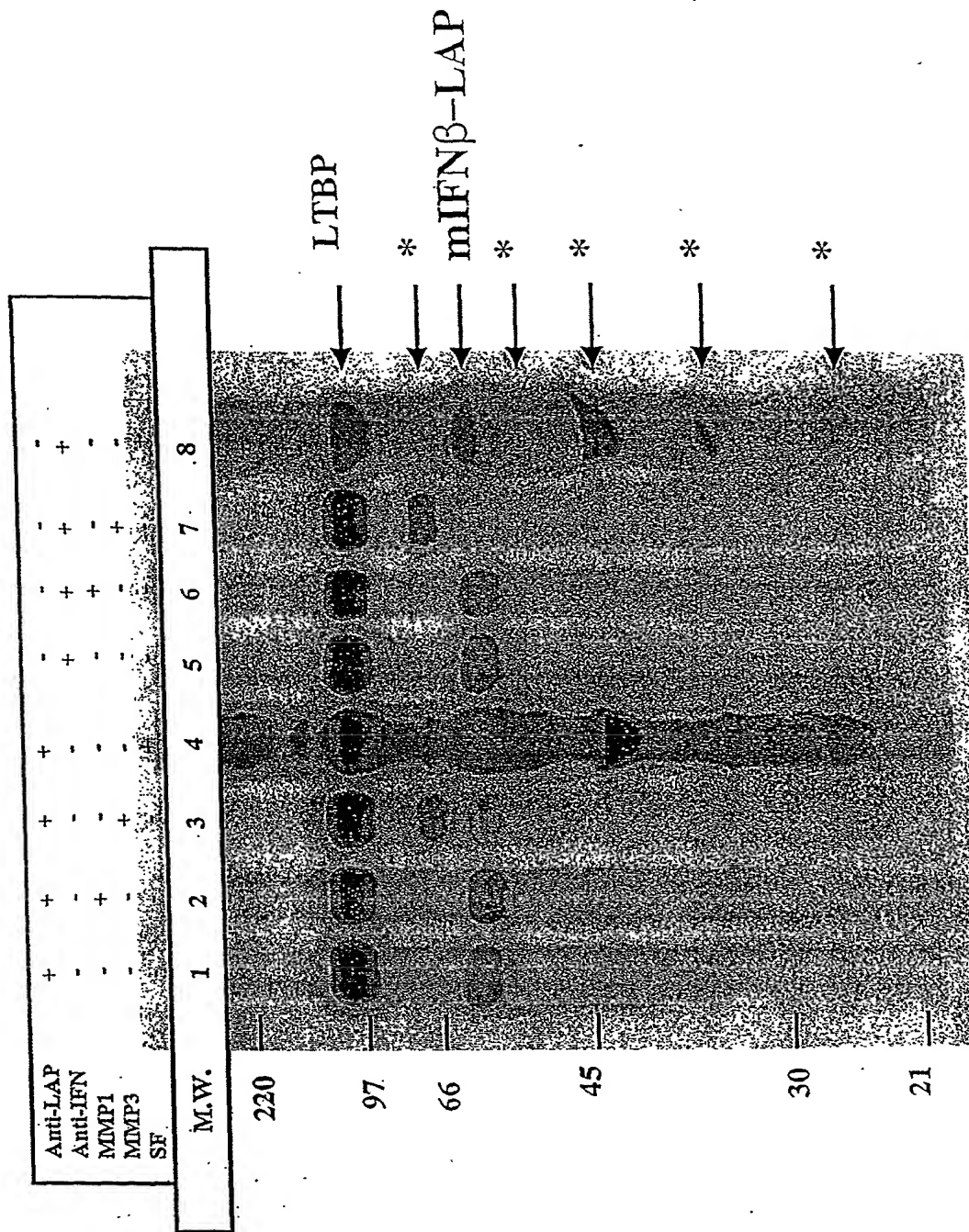
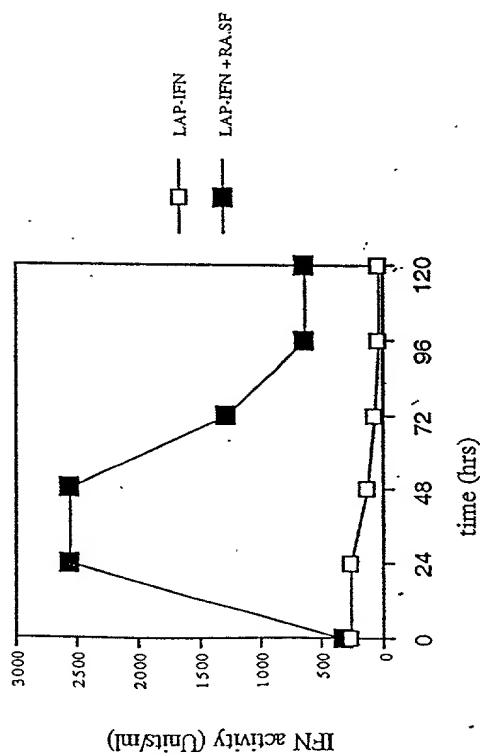


Fig. 8b

A.



B.

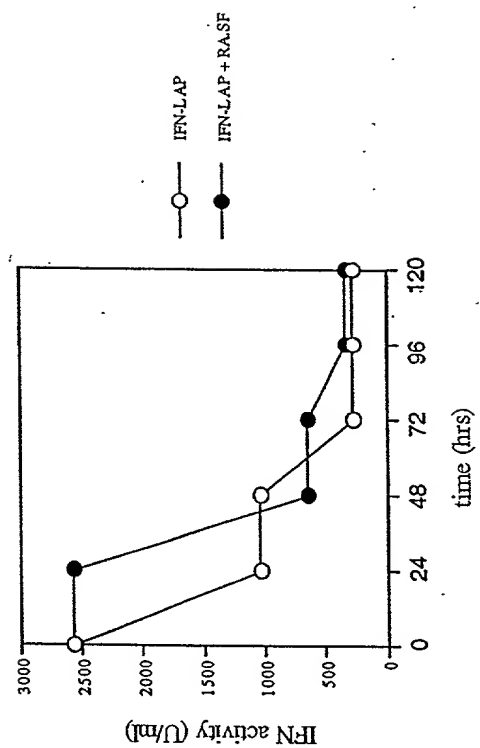
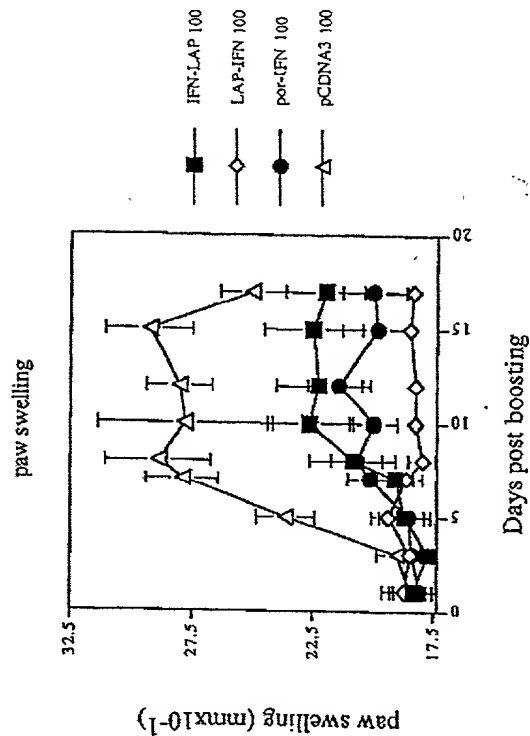


Fig. 9

A.



B.

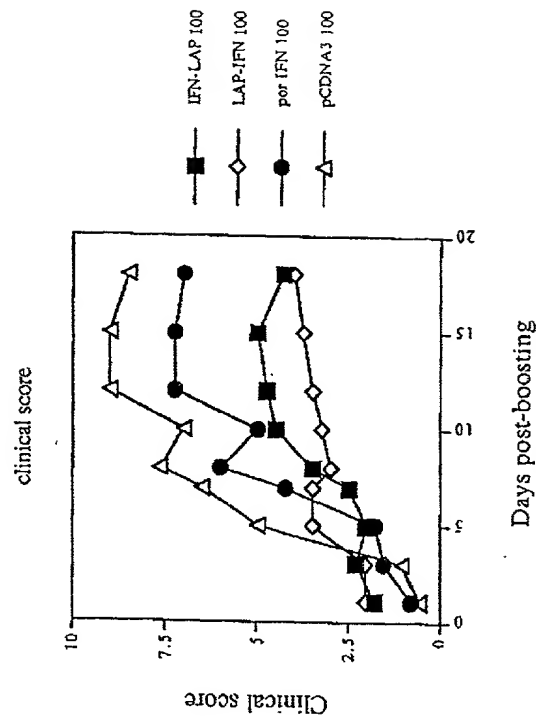


Fig. 10